

Gendore Version 5.1.3
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using sw model

Run On: January 11, 2003, 06:03:32 ; Search time 6157 Seconds
(without alignments)
11211.930 Million cell updates/sec

Title: US-10-005-344-1

Perfect score: 2372

Sequence: 1 gacccgcgagtcggctg.....attacaggcatggccacec 2372

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size :

0

Total number of hits satisfying chosen parameters:

995600

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_ph:*

7: gb_bh:*

8: gb_pl:*

9: qb_dr:*

10: qb_rx:*

11: qb_sts:*

12: qb_sy:*

13: qb_un:*

14: qb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_cv:*

23: em_ph:*

24: em_pl:*

25: em_rn:*

26: em_srs:*

27: em_vl:*

28: em_un:*

29: em_vt:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pln:*

35: em_htg_rdn:*

36: em_htg_mam:*

37: em_htg_vrt:*

38: em_sy:*

39: em_htgo_hum:*

40: em_htgo_mus:*

41: em_htgo_other:*

Length of query on 100% matches

Result No.	Score	Query Length	Match Length	ID	Description	
1	47	2.0	90	9 HUMLDLRFL	K03555 Human low d	
2	43	1.8	80	9 HUMBKFAC	M36133 Human alpha	
3	43	1.8	92	6 AX197472 Sequence	M3132 Human alpha	
4	39	1.6	80	9 HUMBKFAB	AR051522 Sequence	
5	39	1.6	85	6 AR072662 Sequence	AR072662 Sequence	
6	39	1.6	85	6 AR072662 Sequence	AR072662 Sequence	
7	39	1.6	85	6 AR072607 Sequence	M36131 Human alpha	
8	38	1.6	80	9 HUMBKFAA	AR158065 Sequence	
9	37	1.6	51	6 AX161490 Sequence	AX161490 Sequence	
10	37	1.6	51	6 AX162420 Sequence	AX162420 Sequence	
c	11	37	1.6	90	9 HUMLDLRM	M15365 Human low d
c	12	37	1.6	90	9 HUMLDLRM	M15365 Human low d
c	13	37	1.6	94	6 AX197487 Sequence	AX197487 Sequence
c	14	36	1.5	51	6 AX161652 Sequence	AX161652 Sequence
c	15	36	1.5	76	6 A97233 Sequence	A97233 Sequence
c	16	35	1.5	40	6 AR208401 Sequence	AR208401 Sequence
c	17	35	1.5	51	6 AX163202 Sequence	AX163202 Sequence
c	18	35	1.5	70	9 HSLAS32	X91547 H.sapiens D
c	19	34	1.4	51	6 AX159807 Sequence	AX159807 Sequence
c	20	34	1.4	51	6 AX161913 Sequence	AX161913 Sequence
c	21	34	1.4	54	6 AX322189 Sequence	AX322189 Sequence
c	22	32	1.3	51	6 AX157145 Sequence	AX157145 Sequence
c	23	32	1.3	51	6 AX160937 Sequence	AX160937 Sequence
c	24	32	1.3	92	6 AX197468 Sequence	AX197468 Sequence
c	25	32	1.3	94	6 AX197476 Sequence	AX197476 Sequence
c	26	32	1.3	94	6 AX197483 Sequence	AX197483 Sequence
c	27	31	1.3	66	9 AF08751 Homo sapi	AF08751 Homo sapi
c	28	30	1.3	40	6 A68621 Sequence	A68621 Sequence
c	29	30	1.3	51	6 AX156918 Sequence	AX156918 Sequence
c	30	30	1.3	51	6 AX158063 Sequence	AX158063 Sequence
c	31	30	1.3	51	6 AX159555 Sequence	AX159555 Sequence
c	32	30	1.3	51	6 AX190033 Sequence	AX190033 Sequence
c	33	30	1.3	51	9 S62605 C1-Inhibito	S62605 C1-Inhibito
c	34	30	1.3	66	9 HSU67848 Human beta-	U67848 Human beta-
c	35	29	1.2	51	6 AR208404 Sequence	AR208404 Sequence
c	36	29	1.2	51	6 AX118161 Sequence	AX118161 Sequence
c	37	29	1.2	51	6 AX163193 Sequence	AX163193 Sequence
c	38	29	1.2	51	6 AX163312 Sequence	AX163312 Sequence
c	39	29	1.2	60	6 AR051487 Sequence	AR051487 Sequence
c	40	29	1.2	60	6 AR072627 Sequence	AR072627 Sequence
c	41	29	1.2	60	6 AR073172 Sequence	AR073172 Sequence
c	42	29	1.2	76	6 AR051499 Sequence	AR051499 Sequence
c	43	29	1.2	76	6 AR072639 Sequence	AR072639 Sequence
c	44	29	1.2	76	6 AR073184 Sequence	AR073184 Sequence
c	45	29	1.2	88	11 HUMT50563 L30994 Human STS 0	L30994 Human STS 0

ALIGNMENTS

RESULT 1	HUMLDLRFL	HUMAN low density lipoprotein receptor intron A Alu repeat.
LOCUS	K03555	
DEFINITION		
ACCESSION	K03551	
VERSION	GI:187114	
KEYWORDS	Alu repeat; low density lipoprotein receptor-1; repeat region.	
SOURCE	Human DNA.	
ORGANISM	Homo sapiens	
	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteostomi;	
	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	
REFERENCE	Lehrman,M.A., Goldstein,J.L., Russell,D.W. and Brown,M.S.	
AUTHORS	Duplication of seven exons in LDL receptor gene caused by Alu-Alu recombination in a subject with familial hypercholesterolemia	
TITLE	Pred. No. is the number of results predicted by chance to have a	

JOURNAL	Cell 48 (5), 827-835 (1987)	TITLE	Odorant receptor polypeptides and nucleic acids encoding same
MEDLINE	87131094	PATENT	WO 0151632-A 37 19-JUL-2001;
PUBLMED	3815525	LOCATION	Curagen Corporation (US)
COMMENT	Clean copy of sequence kindly provided by M. Lehrman (22-APR-1987).	FEATURES	Location/Qualifiers
SOURCE	1.. .90 /organism="Homo sapiens" /db_xref="taxon:9606" /map="19p1.3" 1 /gene="IDLR" /note="Hgml; G00-119-362" ORIGIN Chromosome 19p13.2-p13.1.	SOURCE	1.. .92 /organism="Homo sapiens" /db_xref="taxon:9606"
misc_feature		BASE COUNT	18 a 23 c 32 g 19 t
BASE COUNT	117 a 30 c 24 g 19 t	Query Match	1.8%; Score 43; DB 6; Length 92;
ORIGIN	Chromosome 19p13.2-p13.1.	Best Local Similarity	100.0%; Pred. No. 1..6e-11;
Query Match	2.0%; Score 47; DB 9; Length 90;	Matches	0; Mismatches 0; Indels 0; Gaps 0;
Best Local Similarity	100.0%; Pred. No. 1..1e-13;	QY	2319 TGATCGGCCACCTCGGGCTCCCAAGTGGGATTAGGG 2361
Matches	47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db	59 TGATCGGCCACCTCGGGCTCCCAAGTGGGATTAGGG 17
RESULT 2		RESULT 4	
LOCUS	HUMBRKFC	LOCUS	HUMBRKFB
DEFINITION	Human alpha-galactosidase break point region.	DEFINITION	Human alpha-galactosidase break point junction; glycosphingolipid catabolism.
VERSION	M36133	VERSION	M36132
KEYWORDS	Fabry disease; break point junction; glycosphingolipid catabolism.	KEYWORDS	Fabry disease; break point junction; glycosphingolipid catabolism.
ORGANISM	Homo sapiens	ORGANISM	Homo sapiens
REFERENCE	Kornreich, R., Bishop,D.F. and Desnick, R.J. 1 (bases 1 to 80)	REFERENCE	Kornreich, R., Bishop,D.F. and Desnick, R.J. Alpha-galactosidase A gene rearrangements causing Fabry disease.
AUTHORS		AUTHORS	
TITLE	Identification of short direct repeats at breakpoints in an Alu-rich gene	TITLE	Identification of short direct repeats at breakpoints in an Alu-rich gene
JOURNAL	J. Biol. Chem. 265 (16), 9319-9326 (1990)	JOURNAL	J. Biol. Chem. 265 (16), 9319-9326 (1990)
PUBLMED	90264427	PUBLMED	90264427
FEATURES	Location/Qualifiers	FEATURES	Location/Qualifiers
SOURCE	1.. .80 /organism="Homo sapiens" /db_xref="taxon:9606" 18 a 28 c 17 g 17 t	SOURCE	1.. .80 /organism="Homo sapiens" /db_xref="taxon:9606" 17 a 29 c 16 g 18 t
BASE COUNT		Query Match	1.6%; Score 39; DB 9; Length 80;
ORIGIN		Best Local Similarity	100.0%; Pred. No. 2..6e-09;
Query Match	1.8%; Score 43; DB 9; Length 80;	Matches	0; Mismatches 0; Indels 0; Gaps 0;
Best Local Similarity	100.0%; Pred. No. 1..7e-11;	QY	2334 GGCTCCAAAGTCCTGGATTACAGGCATAGGCCACCG 2372
Matches	43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db	21 GGCTCCAAAGTCCTGGATTACAGGCATAGGCCACCG 59
RESULT 3		RESULT 5	
LOCUS	AX197472/c	LOCUS	AR051522
DEFINITION	Sequence 37 from Patent WO0151632.	DEFINITION	Sequence 92 from patent US 5830670.
ACCESSION	AX197472	ACCESSION	AR051522
VERSION	AX197472..1	VERSION	AR051522..1
KEYWORDS	human.	KEYWORDS	Unknown.
SOURCE	Homo sapiens	REFERENCE	1 (bases 1 to 85)
ORGANISM	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	AUTHORS	de la Monte,S. and Wands,J.R.
REFERENCE	1 (bases 1 to 92)	TITLE	Neural thread protein gene expression and detection of Alzheimer's disease
AUTHORS	Padigaru,M., Praga,S.K., Taupier,R.J., Mishra,V., Tchernov,V.T., Spytek,K.A. and Li,L.	FEATURES	Patent: US 5830670-A 92 03-NOV-1998; Location/Qualifiers
BASE COUNT	13 a 27 c 25 g 20 t	SOURCE	1.. .85 /organism="unknown"

ORIGIN

Query Match 1.6%; Score 39; DB 6; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2290 GCCAGGATGGTCGATCTCCGTGACCTCGTGTGATCCGCC 2328
Db 9 GCCAGGATGGTCGATCTCCGTGACCTCGTGTGATCCGCC 47

RESULT 6

AR072662 LOCUS AR072662 Sequence 92 from patent US 5948634. DNA linear PAT 28-AUG-2000

DEFINITION Neural thread protein gene expression and detection of alzheimer's disease

VERSION AR072662.1 GI:9999426

KEYWORDS Unknown.

SOURCE Organism:Unclassified.

REFERENCE 1 (bases 1 to 85)
de la Monte,S. and Wands,J.R.

AUTHORS Neural thread protein gene expression and detection of alzheimer's disease

TITLE Patent: US 5948634-A 92 07-SEP-1999;

JOURNAL Location/Qualifiers 1. .85 /organism="unknown"

FEATURES SOURCE 13 a 27 c 25 g 20 t

BASE COUNT ORIGIN

Query Match 1.6%; Score 39; DB 6; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2290 GCCAGGATGGTCGATCTCCGTGACCTCGTGTGATCCGCC 2328
Db 9 GCCAGGATGGTCGATCTCCGTGACCTCGTGTGATCCGCC 47

RESULT 7

AR073207 LOCUS AR073207 Sequence 92 from patent US 5948888. DNA linear PAT 28-AUG-2000

DEFINITION Neural thread protein gene expression and detection of Alzheimer's disease

VERSION AR073207.1 GI:9999970

KEYWORDS Unknown.

SOURCE Organism:Unclassified.

REFERENCE 1 (bases 1 to 85)
de la Monte,S. and Wands,J.R.

AUTHORS Neural thread protein gene expression and detection of Alzheimer's disease

TITLE Patent: US 5948888-A 92 07-SEP-1999;

JOURNAL Location/Qualifiers 1. .85 /organism="unknown"

FEATURES SOURCE 13 a 27 c 25 g 20 t

BASE COUNT ORIGIN

Query Match 1.6%; Score 39; DB 6; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2290 GCCAGGATGGTCGATCTCCGTGACCTCGTGTGATCCGCC 2328
Db 9 GCCAGGATGGTCGATCTCCGTGACCTCGTGTGATCCGCC 47

RESULT 8

HOMBRKFAA

LOCUS HOMBRKFAA Human alpha-galactosidase 80 bp break point region.

DEFINITION Human alpha-galactosidase 80 bp break point region.

ACCESSION M36131

VERSION M36131.1 GI:179541

KEYWORDS Fabry disease; break point junction; glycosphingolipid catabolism.

SOURCE Human DNA.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 80)

AUTHORS Kornreich,R., Bishop,D.F. and Desnick,R.J.

TITLE Alpha-galactosidase A gene rearrangements causing Fabry disease.

FEATURES Identification of short direct repeats at breakpoints in an Alu-rich gene

SOURCE 1. .80 /organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 19 a 28 c 20 g 13 t

ORIGIN

Query Match 1.6%; Score 38; DB 9; Length 80;
Best Local Similarity 100.0%; Pred. No. 9e-09;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2334 GGCCCTCCAAAGTCTGGATTACAGGCATGAGCCAC 2371
Db 21 GGCCCTCCAAAGTCTGGATTACAGGCATGAGCCAC 58

RESULT 9

AX158065 LOCUS AX158065 Sequence 1393 from Patent WO1405211. DNA linear PAT 22-JUN-2001

DEFINITION AX158065

VERSION AX158065.1 GI:14539396

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 51)

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butaleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE Shimkets,R.A. and Leach,M.

FEATURES Nucleic acids containing single nucleotide polymorphisms and methods of use thereof

JOURNAL Patent: WO 0140521-A 1393 07-JUN-2001;

SOURCE Curagen Corporation (US)

BASE COUNT 9 a 21 c 12 g 9 t

ORIGIN

Query Match 1.6%; Score 37; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.3e-08;

Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2318 GTGATCGGCCACCTGGCTCCAAAGTGCGGGAT 2354
Db 15 GTGATCGGCCACCTGGCTCCAAAGTGCGGGAT 51

RESULT 10

AX161490 LOCUS AX161490 Sequence 4818 from Patent WO1405211. DNA linear PAT 22-JUN-2001

DEFINITION

ORIGIN Query Match Similarity 1.6%; Score 37; DB 6; Length 94;
 Best Local Similarity 100.0%; Pred. No. 3.1e-08;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Keywords 0;

LOCUS Sequence AX161652 from Patent WO0140521.
 DEFINITION AX161652 DNA
 ACCESSION AX161652.1 GI:14542983
 VERSION 1
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCES 1 (bases 1 to 51)
 AUTHORS Shunkets, R.A. and Leach, M.
 TITLE Nucleic acids containing single nucleotide polymorphisms and
 methods of use thereof
 JOURNAL Patent: WO 0140521-A 4980 07-JUN-2001;
 FEATURES Curagen Corporation (US)
 Location/Qualifiers 1..51
 SOURCE /organism="Homo sapiens"
 /db_xref="taxon:9606"
 misc_feature 26
 /note="2 of 2 allelic variants (4979 is other entry)
 Accession number SG43979411,
 BASE COUNT 10 a 13 c 17 g 11 t
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 Best Local Similarity 100.0%; Pred. No. 1.2e-07;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Keywords 0;

LOCUS Sequence A97233 from Patent WO9918235.
 DEFINITION A97233 DNA
 ACCESSION A97233.1 GI:6780621
 VERSION 1
 SOURCE unidentified.
 ORGANISM unidentified
 unclassified.
 REFERENCES 1 (bases 1 to 16)
 AUTHORS Abken, H.
 TITLE PROCESSES FOR DETECTING, EXTRACTING OR REMOVING HUMAN OR MAMMALIAN
 CELLS WITH A DISTURBED CELLULAR CYCLE REGULATION OR UNLIMITED
 PROLIFERATION OR TUMOUR-FORMING ABILITY
 JOURNAL Patent: WO 9918235 A 79 15-APR-1999;
 ABKEN HINRICH (DE)
 FEATURES Location/Qualifiers 1..76
 SOURCE /organism="unidentified"
 /db_xref="taxon:32644"
 BASE COUNT 14 a 24 c 22 g 16 t
 ORIGIN Query Match Similarity 1.5%; Score 36; DB 6; Length 76;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;



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OM nucleic - nucleic search, using sw model
Run on: January 11, 2003, 03:27:22 : Search time 490 Seconds
(without alignments)
10901.510 Million cell updates/sec

Title: US-10-005-344-1
Perfect score: 2372
Sequence: 1 gacaccqcgccgacttggctg.....attacaggcatgagccacctg 2372

Scoring table: OLIGO_NDc
Gapext_60.0 , Gapext 60.0

Searched: 2183239 seqs, 1125999159 residues

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 23: /SIDS2/seqdata/geneseq/geneseq/geneseq-emb1/NA2001B.DAT:*
 24: /SIDS2/seqdata/geneseq/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query	Match Length	DB ID	Description
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c 2	60	2.5	60	ABN31842	Human spliced tran
c 3	50	2.1	95	AAC28711	Human secreted pro
c 4	47	2.0	47	AAZ65256	Human map-related
c 5	46	1.9	95	AAK85116	Human secreted pro
c 6	44	1.9	76	AAC15689	Human musculoske
c 7	42	1.8	87	AAL37410	Human nervous syst
c 8	42	1.8	100	ABA22222	Human secreted pro
c 9	41	1.7	86	AA�14994	

ALIGNMENTS

RESULT 1
AX35141/C
ID AX35141 standard; DNA; 73 BP.
XX
AC AX35141;
XX
DT 01-JUL-1999 (first entry)
XX
DE Nucleotide sequence SEQ ID 49.
XX
KW NMD2 protein; antisense oligonucleotide; activate; tumour suppressor;
KW inhibition; tumour growth; DNA-damaging agent; camptothecin;
KW DNA/RNA hybrid; ss.
XX
OS Synthetic.
XX
PN W09910486-A2.
XX
PD 04-MAR-1999.
XX
PF 18-AUG-1998; 98WO-US17147.
XX
PR 06-MAY-1998; 98US-0073567.
PR 22-AUG-1997; 97US-0916384.
PA (HYBR-) HYBRIDON INC.
XX
PI Agrawal, S., Chen, J., Zhang, R;
DR WPI; 1999-254219/21.
XX
PT New NMD2-specific antisense oligonucleotides

XX Disclosure; Page 57; 59pp; English.

PS ABN39842 standard; DNA; 60 BP.

XX ABN39842;

AC DT 15-JUL-2002 (first entry)

XX DE Human spliced transcript detection oligonucleotide SEQ ID NO:12590.

KW Human; mouse; rat; splice variant; transcript; detection; RNA transcript;

KW splice variant; transcriptome; oligonucleotide library; ss.

XX OS Homo sapiens.

XX PN WO200210449-A2.

XX PD 07-FEB-2002.

XX PF 20-JUL-2001; 2001WO-IB01903.

XX PR 28-JUL-2000; 2000US-221607P.

PR 02-MAY-2001; 2001US-287724P.

PA (COMP-) COMPUGEN INC.

XX PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX DR WPI; 2002-257383/30.

XX PT New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and developmental-specific genes.

XX PS Example 1; SEQ ID 12590; 47pp; English.

XX CC The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitative or quantitative characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal

CC transriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue- and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention.

CC N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 73 BP; 17 A; 23 C; 11 G; 22 T; 0 other;

Best Local Similarity 100.0%; Pred. No. 5e-25;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 3.1%; Score 73; DB 20; Length 73;

XX Query Match 2.5%; Score 60; DB 24; Length 60;

Best Local Similarity 100.0%; Pred. No. 1.1e-18;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Qy 98 TGACCGAGACCTGCTGTGCTTTCGAGCAGGGACCGACCCGATATTGCGCTTA 157

Db 1 TGACCGAGATGCTGCTTCGAGCAGGGACCCGATATTGCGCTTA 60

XX Sequence 60 BP; 10 A; 21 C; 16 G; 13 T; 0 other;

XX SQ AAC28711 standard; cDNA; 95 BP.

XX AC AAC28711;

XX DT 06-OCT-2000 (first entry)

XX DE Human secreted protein 5' EST, SEQ ID NO: 32786.

XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.

XX OS Homo sapiens.

XX PN EF033401-A2.

XX PD 06-SEP-2000.

XX PF 21-FEB-2000; 2000EP-0200610.

XX PR 26-FEB-1999; 99US-0122487.

XX PA (GEST) GENSET.

XX PI Dumas Milne Edwards J, Ducleart A, Giordano J;

XX DR WPI; 2000-300381/45.

XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures -

XX PS Claim 1; SEQ ID 32786; 71pp + CD-ROM; English.

XX The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from Oligo dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design

CC expression and secretion vectors.

XX Sequence 95 BP; 18 A; 23 C; 26 G; 28 T; 0 other;

SQ Score 50; DB 21; Length 95;

Query Match 2.1%; Score 50; DB 21; Length 95;

Best Local Similarity 100.0%; Pred. No. 7.8e-14;

Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gaps 0;

Qy 2264 AGTAGAGACAGGGTTTCACCGTGTAGCAGGATGGTCGATCTCTGA 2313

Db 1 AGTAGAGACAGGGTTTCACCGTGTAGCAGGATGGTCGATCTCTGA 50

RESULT 4
AAZ69526 ID AAZ69526 standard; DNA; 47 BP.

XX AC AAK85116;

XX AC AAK85116 standard; DNA; 95 BP.

DE Human map-related biallelic marker SEQ ID NO:3882.

XX Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; diagnosis; single nucleotide polymorphism; SNP; ds.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

FH variation replace(24,T)

FT /*tag= ^a

FT /standard_name= "single nucleotide polymorphism"

XX WO9954500-A2.

PN WO9954500-A2.

PD 28-OCT-1999

XX PF 21-APR-1999; 99WO-TB00822.

XX PR 21-APR-1998; 98US-0082614.

PR 23-NOV-1998; 98US-0109732.

XX PA (GEST) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;

PI DR WPI: 2000-013267/01.

XX PT Novel biallelic markers used to construct a high density disequilibrium map of the human genome

XX PS Claim 3; Page 1058; 2745pp; English.

XX CC AA265654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69573 to AAZ7440 represent amplification primers for the biallelic markers. The biallelic markers of the present invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side effects from pharmaceutical agents acting on a disease as well as other treatment.

CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and 3367, are not actually given a sequence in the Sequence Listing from the present invention.

XX SQ Sequence 47 BP; 8 A; 14 C; 12 G; 13 T; 0 other;

KW Human; 5' EST; expressed sequence tag; secreted protein; CDNA isolation;
 KW gene therapy; chromosome mapping;
 XX ss;

XX Homo sapiens.

OS Homo sapiens.

XX EP1033401-A2.

PN 06-SEP-2000.

PD 21-FEB-2000; 2000EP-0200610.

XX 26-FEB-1999; 99US-012487.

XX (EST) GENSET.

PA Dumas Milne Edwards J, Duclert A, Giordano J;

PR WPI; 2000-500381/45.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -

PS Claim 1; SEQ ID 17764; 71pp + CD-ROM; English.

XX The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or poly+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA
 CC libraries. Such ESTs are well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
 CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors.

XX Sequence 76 BP; 19 A; 19 C; 25 G; 13 T; 0 other;

Query Match 1.9%; score 44; DB 21; Length 76;
 Best Local Similarity 100.0%; Pred. No. 6.3e-11; Mismatches 0; Indels 0; Gaps 0;

Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2285 TCTTAGCCAGGATGGCTCGATCCTGACCTCGTGATCGCCC 2328

Db 76 TCTTAGCCAGGATGGCTCGATCCTGACCTCGTGATCGCCC 33

RESULT 7

AAL3741.0/C

ID AAL37410 standard; DNA: 87 BP.

XX Human musculoskeletal system related polynucleotide SEQ ID NO 3775.

AC AAL37410;

XX DT 08-JAN-2002 (first entry)

XX Human musculoskeletal system related polynucleotide SEQ ID NO 3775.

DE Human musculoskeletal system related polynucleotide SEQ ID NO 3775.

XX Cyostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; antilulcer;
 KW vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein;
 KW musculoskeletal system; ds.

XX Homo sapiens.

OS W0200155367-A1.

PN 02-AUG-2001.

XX 29-SEP-2000; 2000US-0236327.

PR 29-SEP-2000; 2000US-0236367.

PR 29-SEP-2000; 2000US-0236368.

PR 29-SEP-2000; 2000US-0236369.
 PR PT Isolated polypeptide for treating, preventing and/or prognosing
 PR PT disorders related to the musculoskeletal system including
 PR PT musculoskeletal cancers and also for testing and detection e.g.
 PR PT diagnosis -
 XX Example 2; SEQ ID NO 3775; 781pp + Sequence Listing; English.

PR The invention relates to novel genes (AAL34669-AAL37666) and proteins
 PR (ABB01087-ABB04109) associated with the musculoskeletal system useful
 PR for preventing, treating or ameliorating medical conditions e.g. by
 PR protein or gene therapy. The genes are isolated from a range of human
 PR tissues disclosed in the specification. The nucleic acids, proteins,
 PR antibodies and antagonists are useful in the diagnosis treatment,
 PR and prevention of: (a) cancer, e.g. breast and ovarian cancer and
 PR other cancers of the adrenal gland, bone marrow, breast,
 PR gastrointestinal tract, liver, lung, or urogenital; (b) immune
 PR disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 PR anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 PR multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
 PR (c) cardiovascular disorders such as myocardial ischaemias, (d) wound
 PR healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
 PR and (f) infectious diseases such as viral, bacterial, fungal and
 PR parasitic infections.
 PR Note: The sequence data for this patent did not form part of the
 PR printed specification, but was obtained in electronic format directly
 PR from WIPO at ftp://wipo.int/pub/published_pct_sequences.

XX SQ Sequence 87 BP; 19 A; 23 C; 29 G; 16 T; 0 other;

XX Query Match 1.8%; Score 42; DB 22; Length 87;
 XX Best Local Similarity 100.0%; Pred. No. 6.1e-10;
 XX Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2319 TGATCCGCCACCTCGCCGCCAAAGTGCTGGATTACAGG 2360
 Db 48 TGATCCGCCACCTCGCCGCCAAAGTGCTGGATTACAGG 7

RESULT 8
 ID ABA20222 standard; DNA; 100 BP.
 XX ABA20222;
 XX DT 23-JAN-2002 (first entry)
 XX DE Human nervous system related polynucleotide SEQ ID NO 12555.
 XX ID ABA20222 standard; DNA; 100 BP.
 XX KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
 KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; pulmonary;
 KW antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
 KW antirheumatic; hepatotropic; cerebroprotective; antinflammatory;
 KW antiallergic; antidiabetic; antiluler; anticonvulsant; antifungal;
 KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
 XX OS Homo sapiens.
 XX PN WO200159063-A2.
 XX PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.

PI Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-451937/48.
 DR PA (HUMA-) HUMAN GENOME SCI INC.
 XX

PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0215880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0215290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0224513.
 PR 14-AUG-2000; 2000US-0224523.
 PR 14-AUG-2000; 2000US-0224524.
 PR 14-AUG-2000; 2000US-0224529.
 PR 14-AUG-2000; 2000US-0224566.
 PR 14-AUG-2000; 2000US-0224567.
 PR 14-AUG-2000; 2000US-0224568.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225157.
 PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226581.
 PR 22-AUG-2000; 2000US-0226568.
 PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227709.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 05-SEP-2000; 2000US-0229517.
 PR 06-SEP-2000; 2000US-0230437.
 PR 08-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0231415.
 PR 08-SEP-2000; 2000US-0231416.
 PR 12-SEP-2000; 2000US-0231958.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233053.
 PR 14-SEP-2000; 2000US-0233064.
 PR 21-SEP-2000; 2000US-0233055.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234224.
 PR 25-SEP-2000; 2000US-0234937.
 PR 25-SEP-2000; 2000US-0234938.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235836.
 PR 27-SEP-2000; 2000US-0235837.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 13-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.

PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0242221.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 08-NOV-2000; 2000US-0249207.
 PR 08-NOV-2000; 2000US-0249208.
 PR 08-NOV-2000; 2000US-0249209.
 PR 08-NOV-2000; 2000US-0249210.
 PR 08-NOV-2000; 2000US-0249211.
 PR 08-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249219.
 PR 17-NOV-2000; 2000US-0249224.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249246.
 PR 17-NOV-2000; 2000US-0249247.
 PR 17-NOV-2000; 2000US-0249248.
 PR 17-NOV-2000; 2000US-0249249.
 PR 17-NOV-2000; 2000US-0249250.
 PR 17-NOV-2000; 2000US-0249251.
 PR 17-NOV-2000; 2000US-0249252.
 PR 17-NOV-2000; 2000US-0249253.
 PR 17-NOV-2000; 2000US-0249254.
 PR 01-DEC-2000; 2000US-0251160.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251169.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0255097.
 PR 05-JAN-2001; 2001US-0259678.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA PA Barash SC, Ruben SM;
 PI PI Rosen CA, Barash SC, Ruben SM;
 XX XX WPI; 2001-541565/60.
 XX XX Disclosure: SEQ ID NO 12553; 1701PP + Sequence Listing; English.
 PS PS Disclosure: SEQ ID NO 12553; 1701PP + Sequence Listing; English.
 CC CC Nucleic acids encoding 3224 human nervous system antigen polypeptides, and proteins
 PT PT useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification.
 CC CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC CC

CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp://wipo.int/pub/published_pct_sequences.

XX Sequence 100 BP; 22 A; 30 C; 26 G; 22 T; 0 other;

SQ Query Match 1.8%; Score 42; DB 22; Length 100;

Best Local Similarity 100.0%; Pred. No. 6.1e-10; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db Qy 2325 GCCCCACCTGGCCCTCCAAGTGGGGATACAGGATGAG 2366

Db 59 GCCCACCTGGCTCCAAAGTGCTGGATACAGGCATGAG 100

RESULT 9

ID AAC11994 standard; cDNA: 86 BP.

XX AC AAC11994;

XX DT 06-OCT-2000 (first entry)

DE Human secreted protein 5' EST, SEQ ID NO: 19069.

XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

XX KW gene therapy; chromosome mapping; ss.

OS Homo sapiens.

XX PN EP1033401-A2.

XX PD 06-SEP-2000.

XX PF 21-FEB-2000; 20000EP-02000610.

XX PR 26-FEB-1999; 99US-0122487.

XX PA (GEST) GENSET.

XX PI Dumas Milne Edwards J., Duclert A., Giordano J.;

XX WPI; 2000-5000381/45.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX Claim 1; SEQ ID 19069; 71pp + CD-ROM; English.
 PS The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or poly+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from Oligo-dT primed cDNA
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
 CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors.

XX SQ Sequence 86 BP; 24 A; 21 C; 24 G; 17 T; 0 other;	XX SQ Sequence 86 BP; 24 A; 21 C; 24 G; 17 T; 0 other;
Query Match 1.7%; Score 41; DB 21; Length 86;	Query Match 1.7%; Score 41; DB 21; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.9e-09;	Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2284 GTGTAGCCAGGATGGTCTCGATCCTCGTCGATCC 2324	Qy 2284 GTGTAGCCAGGATGGTCTCGATCCTCGTCGATCC 2324
Db 62 GTGTAGCCAGGATGGTCTCGATCCTCGTCGATCC 22	Db 62 GTGTAGCCAGGATGGTCTCGATCCTCGTCGATCC 22
RESULT 10	
AAK8355	AAK8355 standard; DNA: 99 BP.
ID AAK83535	ID AAK83535 standard; DNA: 99 BP.
XX AC AAK83535;	XX AC AAK83535;
XX DT 07-NOV-2001 (first entry)	XX DT 07-NOV-2001 (first entry)
XX DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 38347.	XX DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 38347.
XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;	XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX CYTOSTATIC; gene therapy; vaccine; metastasis; ds.	XX CYTOSTATIC; gene therapy; vaccine; metastasis; ds.
XX OS Homo sapiens.	XX OS Homo sapiens.
XX PN WC200157182-A2.	XX PN WC200157182-A2.
XX PD 09-AUG-2001.	XX PD 09-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US01354.	XX PF 17-JAN-2001; 2001WO-US01354.
XX PR 31-JAN-2000; 2000US-0179065.	XX PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180028.	PR 04-FEB-2000; 2000US-0180028.
PR 24-FEB-2000; 2000US-0184664.	PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.	PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.	PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.	PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.	PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.	PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.	PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214816.	PR 28-JUN-2000; 2000US-0214816.
PR 30-JUN-2000; 2000US-0215135.	PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.	PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.	PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.	PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.	PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.	PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.	PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.	PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.	PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0225213.	PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225757.	PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.	PR 14-AUG-2000; 2000US-0225758.
PR 18-AUG-2000; 2000US-0225759.	PR 18-AUG-2000; 2000US-0225759.
PR 22-AUG-2000; 2000US-0226681.	PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.	PR 22-AUG-2000; 2000US-0226868.
PR 23-AUG-2000; 2000US-0227102.	PR 23-AUG-2000; 2000US-0227102.
PR 30-AUG-2000; 2000US-0227099.	PR 30-AUG-2000; 2000US-0227099.
PR 01-SEP-2000; 2000US-0229281.	PR 01-SEP-2000; 2000US-0229281.
PR 01-SEP-2000; 2000US-0229343.	PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229345.	PR 01-SEP-2000; 2000US-0229345.

PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-023080.
 PR 08-SEP-2000; 2000US-023081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0233397.
 PR 14-SEP-2000; 2000US-0233398.
 PR 14-SEP-2000; 2000US-0233399.
 PR 14-SEP-2000; 2000US-0234001.
 PR 14-SEP-2000; 2000US-0234063.
 PR 14-SEP-2000; 2000US-0234064.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0234984.
 PR 27-SEP-2000; 2000US-0235134.
 PR 27-SEP-2000; 2000US-0238336.
 PR 29-SEP-2000; 2000US-0235327.
 PR 29-SEP-2000; 2000US-0236167.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 02-OCT-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236002.
 PR 02-OCT-2000; 2000US-023037.
 PR 02-OCT-2000; 2000US-0231038.
 PR 02-OCT-2000; 2000US-0231039.
 PR 13-OCT-2000; 2000US-023040.
 PR 13-OCT-2000; 2000US-0230935.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0241617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.

PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0251391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Rosen CA, Barash SC, Ruben SM:
 XX XX Disclosure; SEQ ID NO 38347; 3071pp + Sequence Listing; English.
 XX WPI; 2001-483426/52.
 DR XX
 XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis -
 XX PT supplement the patients own production of (I). Additionally, (I)
 PS CC poly nucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and poly nucleotides may be used to prevent,
 CC diagnose and treat immune/haematoepoietic-related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC sequences from the present invention AAK64942 to AAK54950 and AAM82169
 CC represent sequences used in the exemplification of the present invention.
 XX SQ sequence 99 BP; 19 A; 33 C; 27 G; 20 T; 0 other;
 XX Query Match 1.7%; Score 40; DB 22; Length 99;
 XX Best Local Similarity 100.0%; Pred. No. 5.7e-09;
 XX Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2330 CCTCGGCCCTCCAAAGTGCCTGGATTACGGCATGAGCCA 2369
 ID XX AAK86591 standard; DNA; 99 bp.
 AC XX AAK86591;
 Db 60 CCTCGGCCCTCCAAAGTGCCTGGATTACGGCATGAGCCA 99

RESULT 11
 AAK86591
 ID AAK86591
 XX
 AC
 Db 07-NOV-2001 (First entry)

DE	Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41403.	PR	21-SEP-2000;
XX	KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;	PR	21-SEP-2000;
KW	cystostatic; gene therapy; vaccine; metastasis; ds.	PR	25-SEP-2000;
XX		PR	25-SEP-2000;
OS	Homo sapiens.	PR	26-SEP-2000;
XX	WO200157182-A2.	PR	27-SEP-2000;
PN		PR	27-SEP-2000;
XX		PR	29-SEP-2000;
PD	09-AUG-2001.	PR	29-SEP-2000;
XX	PF 17-JAN-2001; 2001WO-US01354.	PR	29-SEP-2000;
XX	PR 31-JAN-2000; 2000US-0179065.	PR	02-OCT-2000;
PR	04-FEB-2000; 2000US-0180628.	PR	02-OCT-2000;
PR	24-FEB-2000; 2000US-0184664.	PR	02-OCT-2000;
PR	02-MAR-2000; 2000US-0186150.	PR	02-OCT-2000;
PR	16-MAR-2000; 2000US-0189874.	PR	02-OCT-2000;
PR	17-MAR-2000; 2000US-0190076.	PR	13-OCT-2000;
PR	18-APR-2000; 2000US-0198123.	PR	13-OCT-2000;
PR	19-MAY-2000; 2000US-0205115.	PR	20-OCT-2000;
PR	07-JUN-2000; 2000US-0203467.	PR	20-OCT-2000;
PR	28-JUN-2000; 2000US-0214886.	PR	20-OCT-2000;
PR	30-JUN-2000; 2000US-0215135.	PR	20-OCT-2000;
PR	07-JUL-2000; 2000US-0216847.	PR	20-OCT-2000;
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PR	14-JUL-2000; 2000US-0217496.	PR	20-OCT-2000;
PR	26-JUL-2000; 2000US-0218290.	PR	20-OCT-2000;
PR	26-JUL-2000; 2000US-0220963.	PR	08-NOV-2000;
PR	14-AUG-2000; 2000US-0220964.	PR	08-NOV-2000;
PR	14-AUG-2000; 2000US-0224518.	PR	08-NOV-2000;
PR	14-AUG-2000; 2000US-0224519.	PR	08-NOV-2000;
PR	14-AUG-2000; 2000US-0225131.	PR	08-NOV-2000;
PR	14-AUG-2000; 2000US-0225134.	PR	08-NOV-2000;
PR	14-AUG-2000; 2000US-0225158.	PR	08-NOV-2000;
PR	14-AUG-2000; 2000US-0225166.	PR	08-NOV-2000;
PR	14-AUG-2000; 2000US-0225167.	PR	08-NOV-2000;
PR	18-AUG-2000; 2000US-0225168.	PR	08-NOV-2000;
PR	14-AUG-2000; 2000US-0225270.	PR	08-NOV-2000;
PR	14-AUG-2000; 2000US-0225447.	PR	08-NOV-2000;
PR	14-AUG-2000; 2000US-0225454.	PR	08-NOV-2000;
PR	14-AUG-2000; 2000US-0225577.	PR	08-NOV-2000;
PR	14-AUG-2000; 2000US-0225758.	PR	08-NOV-2000;
PR	14-AUG-2000; 2000US-0225759.	PR	08-NOV-2000;
PR	18-AUG-2000; 2000US-0226179.	PR	08-NOV-2000;
PR	22-AUG-2000; 2000US-0226681.	PR	08-NOV-2000;
PR	22-AUG-2000; 2000US-0226868.	PR	08-NOV-2000;
PR	22-AUG-2000; 2000US-0227182.	PR	17-NOV-2000;
PR	23-AUG-2000; 2000US-0227009.	PR	17-NOV-2000;
PR	30-AUG-2000; 2000US-0228924.	PR	17-NOV-2000;
PR	01-SEP-2000; 2000US-0229987.	PR	17-NOV-2000;
PR	06-SEP-2000; 2000US-0230437.	PR	17-NOV-2000;
PR	08-SEP-2000; 2000US-0230438.	PR	17-NOV-2000;
PR	01-SEP-2000; 2000US-0229444.	PR	17-NOV-2000;
PR	01-SEP-2000; 2000US-0223345.	PR	17-NOV-2000;
PR	05-SEP-2000; 2000US-0225059.	PR	17-NOV-2000;
PR	05-SEP-2000; 2000US-0229513.	PR	17-NOV-2000;
PR	08-SEP-2000; 2000US-0231413.	PR	17-NOV-2000;
PR	08-SEP-2000; 2000US-0231414.	PR	17-NOV-2000;
PR	08-SEP-2000; 2000US-0232080.	PR	17-NOV-2000;
PR	08-SEP-2000; 2000US-0230438.	PR	17-NOV-2000;
PR	08-SEP-2000; 2000US-0231242.	PR	17-NOV-2000;
PR	12-SEP-2000; 2000US-0231243.	PR	17-NOV-2000;
PR	14-SEP-2000; 2000US-0231244.	PR	17-NOV-2000;
PR	08-SEP-2000; 2000US-0231413.	PR	17-NOV-2000;
PR	14-SEP-2000; 2000US-0233398.	PR	17-NOV-2000;
PR	14-SEP-2000; 2000US-0232199.	PR	17-NOV-2000;
PR	14-SEP-2000; 2000US-0232400.	PR	17-NOV-2000;
PR	14-SEP-2000; 2000US-023401.	PR	17-NOV-2000;
PR	14-SEP-2000; 2000US-0233653.	PR	17-NOV-2000;
PR	14-SEP-2000; 2000US-0233664.	PR	17-NOV-2000;
PR	14-SEP-2000; 2000US-0233365.	PR	17-NOV-2000;

PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI; 2001-183426/52.
 XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides, metasta^sis -
 PT met for preventing, diagnosing and/or treating cancers and
 PT metastasis -
 XX Disclosure; SEQ ID NO 41403; 3071pp + Sequence Listing; English.
 XX AAK4951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytosatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased,
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic -related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC to AAK7694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK4942 to AAK54950 and AAM82169
 CC represent sequences used in the exemplification of the present invention.
 XX Sequence 99 BP; 19 A; 33 C; 27 G; 20 T; 0 other;
 SQ Query Match 1.7%; Score 40; DB 22; Length 99;
 Best Local Similarity 100.0%; Pred. No. 5.7e-09;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AC
 Qy 2330 CCTGGCCTCCAAAGTGTGGATTACGGCATGAGCCA 2369
 Db 60 CCTCGGCCTCCAAAGTGTGGATTACGGCATGAGCCA 99
 DT 06-OCT-2000 (first entry)
 XX Human secreted protein 5' EST, SEQ ID NO: 18764.
 DE Human; 5' EST; expressed sequence tag; secreted protein; cdNA isolation;
 KW gene therapy; chromosome mapping; ss.
 XX
 RESULT 12
 AAC14830
 ID AAC14830 standard; cdNA; 99 BP.
 XX
 AC AAC14830;
 XX
 DT 06-OCT-2000 (first entry)
 XX Human secreted protein 5' EST, SEQ ID NO: 18905.
 DE Human; 5' EST; expressed sequence tag; secreted protein; cdNA isolation;
 KW gene therapy; chromosome mapping; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1033401-A2.
 XX
 PD 06-SEP-2000.
 XX 21-FEB-2000; 2000EP-0200610.
 PR 26-FEB-1999; 99US-0122487.
 PA (GEST) GENSET.
 XX Dumas Milne Edwards J, Duclert A, Giordano J;
 PI Dumas Milne Edwards J, Duclert A, Giordano J;
 XX
 DR WPI; 2000-500381/45.
 XX
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX
 Claim 1; SEQ ID 18764; 71pp + CD-ROM; English.
 XX
 CC The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)

PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-023080.
 PR 08-SEP-2000; 2000US-023081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0233398.
 PR 14-SEP-2000; 2000US-0231399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-023063.
 PR 14-SEP-2000; 2000US-0231064.
 PR 14-SEP-2000; 2000US-023065.
 PR 21-SEP-2000; 2000US-0231223.
 PR 21-SEP-2000; 2000US-0231224.
 PR 25-SEP-2000; 2000US-0231997.
 PR 25-SEP-2000; 2000US-0231998.
 PR 26-SEP-2000; 2000US-0233484.
 PR 27-SEP-2000; 2000US-0233634.
 PR 27-SEP-2000; 2000US-0233836.
 PR 29-SEP-2000; 2000US-0231627.
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 PR 29-SEP-2000; 2000US-0231629.
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 PR 13-OCT-2000; 2000US-0233935.
 PR 13-OCT-2000; 2000US-0339337.
 PR 20-OCT-2000; 2000US-0241960.
 PR 20-OCT-2000; 2000US-0241221.
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 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.

PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249665.
 PR 17-NOV-2000; 2000US-0249675.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250191.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-483426/52.
 XX Disclosure: SEQ ID NO 39925; 3071PB + Sequence Listing; English.
 XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis
 XX PT
 PT
 PT
 PT
 XX DR
 XX PS
 XX XX
 XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I) amino acid sequences given in AAK82170 to AAK91921. (I) have cytotoxic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patient's own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/hematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK5394 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
 XX SQ Sequence 98 BP; 18 A; 27 C; 36 G; 17 T; 0 Other;
 Query Match 1.6%; Score 38; DB 22; Length 98;
 Best Local Similarity 100.0%; Pred. No. 5, 4e-08;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 50 Gccctcccaaaatggattacaggcatgagccacc 2371
 Qy 2334 GGCCCTCCAAAGTGTGGATTACAGGCATGAGCACC 2371
 Db 50 Gccctcccaaaatggattacaggcatgagccacc 13
 Search completed: January 11, 2003, 07:12:37
 Job time : 492 secs



GenCore version 5.1.3 Copyright (C) 1993 - 2003 CompuGen Ltd.	nucleic - nucleic search, using sw model	January 11, 2003, 06:05:17 ; Search time 88 Seconds (without alignments) 8266.333 Million cell updates/sec	US-10-005-344-1 2372 1 gcacgcgcgatgtggctg.....attacaggcattaggccaccc 2372	441362 seqs, 153338381 residues	0	total number of hits satisfying chosen parameters: 687286
Result 1 US-03-072 567 49/c ; Sequence 49, Application US/09073567 ; Patent No. 6013786	GENERAL INFORMATION: ; APPLICANT: Jiandong Chen ; APPLICANT: Sudhir Agrawal ; APPLICANT: Ruiwen Zhang ; TITLE OF INVENTION: MDM2-SPECIFIC ANTISENSE OLIGONUCLEOTIDES ; NUMBER OF SEQUENCES: 49 ; CORRESPONDENCE ADDRESS: ; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff ; STREET: 300 South Wacker Drive, 32nd Floor ; CITY: Chicago ; STATE: IL ; COUNTRY: United States of America ; ZIP: 60606	Operating System: PC-DOS/MS-DOS CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/073,567 FILING DATE: CLASSIFICATION: ATTORNEY/AGENT INFORMATION: NAME: Greenfield, Michael S. REGISTRATION NUMBER: 37,147 REFERENCE/DOCKET NUMBER: 98,057-A TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 913-0001 TELEFAX: (312) 913-0002 INFORMATION FOR SEQ ID NO: 49: SEQUENCE CHARACTERISTICS: LENGTH: 73 base pairs TYPE: nucleic acid STRANDEDNESS: both TOPOLOGY: linear MOLECULE TYPE: nucleic acid HYDROPHOBICITY: NO ANTI-SENSE: YES	ALIGNMENTS	RESULT 1 US-03-072 567 49/c ; Sequence 49, Application US/09073567 ; Patent No. 6013786	SEQUENCE 1, Appl SEQUENCE 2, Appl SEQUENCE 3, Appl SEQUENCE 4, Appl SEQUENCE 5, Appl SEQUENCE 6, Appl SEQUENCE 7, Appl SEQUENCE 8, Appl SEQUENCE 9, Appl SEQUENCE 10, Appl SEQUENCE 11, Appl SEQUENCE 12, Appl SEQUENCE 13, Appl SEQUENCE 14, Appl SEQUENCE 15, Appl SEQUENCE 16, Appl SEQUENCE 17, Appl SEQUENCE 18, Appl SEQUENCE 19, Appl SEQUENCE 20, Appl SEQUENCE 21, Appl SEQUENCE 22, Appl	0
Summary	Issued_Patents_NA: 1: /cgn2_6/pctodata/2/ina/5A_COMB_seq.* 2: /cgn2_6/pctodata/2/ina/5B_COMB_seq.* 3: /cgn2_6/pctodata/2/ina/6A_COMB_seq.* 4: /cgn2_6/pctodata/2/ina/6B_COMB_seq.* 5: /cgn2_6/pctodata/2/ina/pctus_COMB_seq.* 6: /cgn2_6/pctodata/2/ina/backfile1.seq.*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	RESULTS	Score 73; DB 3; Length 73; Best Local Similarity 100.0%; Pred. No. 6.7e-0; Matches 73; Conservative 0; Mismatches 0-0; Indels 0; Gaps 0;	QY 665 AGGTACATCTGTAGTGTAGAACAGGTGTCACCTGAAAGTCGAGCTAAAGACCT 724	
Summary	Score 73; DB 3; Length 73; Best Local Similarity 100.0%; Pred. No. 6.7e-0; Matches 73; Conservative 0; Mismatches 0-0; Indels 0; Gaps 0;	Score 73; DB 3; Length 73; Best Local Similarity 100.0%; Pred. No. 6.7e-0; Matches 73; Conservative 0; Mismatches 0-0; Indels 0; Gaps 0;	Score 73; DB 3; Length 73; Best Local Similarity 100.0%; Pred. No. 6.7e-0; Matches 73; Conservative 0; Mismatches 0-0; Indels 0; Gaps 0;	Score 73; DB 3; Length 73; Best Local Similarity 100.0%; Pred. No. 6.7e-0; Matches 73; Conservative 0; Mismatches 0-0; Indels 0; Gaps 0;	QY 665 AGGTACATCTGTAGTGTAGAACAGGTGTCACCTGAAAGTCGAGCTAAAGACCT 724	

Db 73 AGGTACATCTGAGTGGAAACAGGTGTCACCTGAAGTGGAGTCAAAAGGACCT 14

QY 725 TGTACAAGAGCCT 737

Db 13 TGTACAAGAGCCT 1

RESULT 2

US-08-454-557C-92 Sequence 92, Application US/08454557C

; Patent No. 5830570

; GENERAL INFORMATION:

; APPLICANT: de la Monte, Suzanne

; APPLICANT: Wands, Jack R.

; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection

; TITLE OF INVENTION: of Alzheimer's Disease

; NUMBER OF SEQUENCES: 121

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

; STREET: 110 New York Avenue, Suite 600

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/454,557C

; FILING DATE: 30-MAY-1995

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Ludwig, Steven R.

; REGISTRATION NUMBER: 36,203

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540

; INFORMATION FOR SEQ ID NO: 92:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 85 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: both

; TOPOLOGY: both

; US-08-454-557C-92

Query Match 1.6%; Score 39; DB 2; Length 85;

Best Local Similarity 100.0%; Pred. No. 2.2e-08;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; Qy 2290 GCCAGGATGGTCGATCTCGACTCTGACCTCGTGATCCGCC 2328

; Db 9 GCGAGGATGGTCGATCTCGACTCTGACCTCGTGATCCGCC 47

; RESULT 4

US-08-450-673C-92 Sequence 92, Application US/08450673C

; Patent No. 5948388

; GENERAL INFORMATION:

; APPLICANT: de la Monte, Suzanne

; APPLICANT: Wands, Jack R.

; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection

; TITLE OF INVENTION: of Alzheimer's Disease

; NUMBER OF SEQUENCES: 121

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

; STREET: 110 New York Avenue, Suite 600

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/450,673C

; FILING DATE: 30-MAY-1995

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Ludwig, Steven R.

; REGISTRATION NUMBER: 36,203

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540

; INFORMATION FOR SEQ ID NO: 92:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 85 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: both

; TOPOLOGY: both

;

US-08-450-673C-92
Query Match Score 1.6%; Score 39; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2290 GCCAGGATGGCTCATCTGATCTCGACCTCGTGAATCCGC 2328
Db 9 GCCAGGATGGCTCATCTGATCTCGACCTCGTGAATCCGCC 47

RESULT 5
PCT US93-17111A-92
; Sequence 92, Application PC/TUS9517111A
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Lands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20005-3034
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/TUS95/17111A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/340,426
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609 38400002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 85 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
PCT-US95-17111A-92

Query Match Score 1.6%; Score 39; DB 5; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2290 GCCAGGATGGCTCATCTGATCTCGACCTCGTGAATCCGC 2328
Db 9 GCCAGGATGGCTCATCTGATCTCGACCTCGTGAATCCGCC 47

RESULT 6
US-09-510-699-17
; Sequence 17, Application US/09540699
; Patent No. 638752
; GENERAL INFORMATION:
; APPLICANT: Agrawal, Sudhir
; APPLICANT: Kandimalla, Ekambar R.
; TITLE OF INVENTION: Pseudo-Cyclic Oligonucleobases
; FILE REFERENCE: 99,128-B
; CURRENT APPLICATION NUMBER: US/09/540,699

CURRENT FILING DATE: 2000-03-31
; PRIORITY NUMBER: US 60/127,138
; PRIOR FILING DATE: 1999-03-31
; PRIORITY NUMBER: US 60/174,642
; PRIORITY NUMBER: 2000-01-05
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 17
; LENGTH: 40
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Oligonucleotide
; OTHER INFORMATION: that is complementary to a portion of the human
; OTHER INFORMATION: mRNA
US-09-540-699-17

RESULT 7
US-09-060-023A-1/C
; Sequence 1, Application US/09060023A
; Patent No. 6301642
; GENERAL INFORMATION:
; APPLICANT: Resnick, Michael A.
; APPLICANT: Larionov, Vladimir L.
; APPLICANT: Kouprieva, Natalya Y.
; APPLICANT: Perkins, Edith L.
; TITLE OF INVENTION: TRANSFORMATION-ASSOCIATED RECOMBINATION
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Needle & Rosenberg, P.C.
; STREET: Suite 1200, 127 Peachtree Street, N.E.
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,023A
; FILING DATE: April 14, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/11478
; FILING DATE: JULY 9, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perryman, David G.
; REGISTRATION NUMBER: 33,438
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-688-0770
; TELEFAX: 404-688-9880
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-060-023A-1

Query Match Score 30; DB 4; Length 40;

Best Local Similarity 100.0%; Pred. No. 0.00029;
 Matches 30; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

RESULT 8
 US-09-540-699-20/C
 ; Sequence 20, Application US/09540699
 ; GENERAL INFORMATION:
 ; APPLICANT: Agrawal, Sudhir
 ; Kandimalla, Ekandar R.
 ; TITLE OF INVENTION: Pseudo-cyclic Oligonucleobases
 ; FILE REFERENCE: 99-128-B
 ; CURRENT APPLICATION NUMBER: US/09/540,699
 ; CURRENT FILING DATE: 2000-03-31
 ; PRIOR APPLICATION NUMBER: US 60/127,138
 ; PRIOR FILING DATE: 1999-03-31
 ; PRIOR APPLICATION NUMBER: US 60/174,642
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 20
 ; LENGTH: 29
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: MDM2 mRNA
 ; OTHER INFORMATION: probe; +338 to +389.
 ; US-09-540-699-20

Query Match 1.2%; Score 29; DB 2; Length 60;
 Best Local Similarity 100.0%; Pred. No. 0.00081;
 Matches 29; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

RESULT 9
 US-08-454-557C-57
 ; Sequence 57, Application US/0845457C
 ; Patent No. 5830670
 ; GENERAL INFORMATION:
 ; APPLICANT: de la Monte, Suzanne
 ; Wands, Jack R.
 ; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
 ; NUMBER OF SEQUENCES: 121
 ; TITLE OF INVENTION: of Alzheimer's Disease
 ; NUMBER OF SEQUENCES: 121
 ; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
 ; NUMBER OF SEQUENCES: 121
 ; TITLE OF INVENTION: of Alzheimer's Disease
 ; NUMBER OF SEQUENCES: 121
 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
 ; STREET: 1100 New York Avenue, Suite 600
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/340,426D
 ; FILING DATE: 14-NOV-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ludwig, Steven R.
 ; REGISTRATION NUMBER: 36,203
 ; REFERENCE/DOCKET NUMBER: 0609_3840002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 371-2600
 ; TELEFAX: (202) 371-2540
 ; INFORMATION FOR SEQ ID NO: 57:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 60 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: both
 ; US-08-454-557C-57

Query Match 1.2%; Score 29; DB 2; Length 60;
 Best Local Similarity 100.0%; Pred. No. 0.00081;
 Matches 29; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

RESULT 11
 US-08-450-673C-57
 ; Sequence 57, Application US/08450673C

Patent No. 5948888
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US08/450,673C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE DOCKET NUMBER: 0609.3840004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
US-08-450-673C-57

Query Match 1.2%; Score 29; DB 2%; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 29; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

RESULT 12
PCT-US95-1711A-57
Sequence 57, Application PC/TUS951711A
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and
Detection of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE DOCKET NUMBER: 0609.3840003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
US-08-454-557C-69

Query Match 1.2%; Score 29; DB 2%; Length 76;
Best Local Similarity 100.0%; Pred. No. 0.0008;
Matches 29; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

RESULT 13
US-08-454-557C-69
Sequence 69, Application US/0845457C
Patent No. 5830670
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE DOCKET NUMBER: 0609.3840003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
US-08-454-557C-69

Query Match 1.2%; Score 29; DB 2%; Length 76;
Best Local Similarity 100.0%; Pred. No. 0.0008;
Matches 29; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 2260 TTTAGTAGAGACAGGGTTACCGTGT 2288
Db 25 TTTATGAGACAGGGTTACCGTGT 53

RESULT 14
US-08-454-557C-69
Sequence 69, Application US/0845457C
Patent No. 5830670
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and
Detection of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE DOCKET NUMBER: 0609.3840003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
US-08-454-557C-69

Query Match 1.2%; Score 29; DB 2%; Length 76;
Best Local Similarity 100.0%; Pred. No. 0.0008;
Matches 29; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 2260 TTTAGTAGAGACAGGGTTACCGTGT 2288
Db 25 TTTATGAGACAGGGTTACCGTGT 53

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 11, 2003, 06:08:32 ; Search time 108 Seconds
(without alignments)
9665.973 Million cell updates/sec

Title: US-10-005-344-1
Perfect score: 2372
Sequence: 1 gacccggcgagttggctg attacaggatggccaccg 2372

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 389086 seqs, 220051671 residues

Word size : 0

Total number of hits satisfying chosen parameters: 239302

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA:
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 2: /cgn2_6/piodata/2/pubpna/pct_new_pub_seq;*
 3: /cgn2_6/piodata/2/pubpna/us06_new_pub_seq;*
 4: /cgn2_6/piodata/2/pubpna/us05_pubcomb.seq;*
 5: /cgn2_6/piodata/2/pubpna/us07_new_pub_seq;*
 6: /cgn2_6/piodata/2/pubpna/pctus_pubcomb.seq;*
 7: /cgn2_6/piodata/2/pubpna/us08_new_pub_seq;*
 8: /cgn2_6/piodata/2/pubpna/us09_pubcomb.seq;*
 9: /cgn2_6/piodata/2/pubpna/us09_new_pub_seq;*
 10: /cgn2_6/piodata/2/pubpna/us10_new_pub_seq;*
 11: /cgn2_6/piodata/2/pubpna/us10_pubcomb.seq;*
 12: /cgn2_6/piodata/2/pubpna/us60_new_pub_seq;*
 13: /cgn2_6/piodata/2/pubpna/us60_pubcomb.seq;*
 14: /cgn2_6/piodata/2/pubpna/us62_pubcomb.seq;*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	43	1.8	92	10 US-09-761-288-37	Sequence 37, Appl
c 2	42	1.8	87	10 US-09-764-877-3775	Sequence 3775, Appl
c 3	37	1.6	94	10 US-09-761-288-33	Sequence 33, Appl
c 4	32	1.3	94	10 US-09-761-288-41	Sequence 4, Appl
c 5	32	1.3	92	10 US-09-761-288-33	Sequence 33, Appl
c 6	32	1.3	94	10 US-09-761-288-48	Sequence 48, Appl
c 7	29	1.2	96	10 US-09-761-288-47	Sequence 47, Appl
c 8	29	1.2	98	10 US-09-764-847-1866	Sequence 1866, Appl
c 9	29	1.2	98	10 US-09-764-847-1867	Sequence 1867, Appl
c 10	28	1.2	28	10 US-09-225-201-27	Sequence 27, Appl
c 11	28	1.2	28	10 US-09-225-201-28	Sequence 28, Appl
c 12	28	1.2	84	10 US-09-920-300A-1278	Sequence 1278, Appl
c 13	28	1.2	84	12 US-10-033-528-1278	Sequence 1278, Appl
c 14	28	1.2	88	10 US-09-764-869-1719	Sequence 1719, Appl
c 15	27	1.1	84	10 US-09-764-860-1053	Sequence 1053, Appl
c 16	27	1.1	84	10 US-09-764-860-1052	Sequence 1052, Appl
c 17	27	1.1	87	10 US-09-764-869-1866	Sequence 1866, Appl
c 18	27	1.1	87	10 US-09-764-860-166	Sequence 166, Appl
c 19	27	1.1	87	10 US-09-764-860-962	Sequence 962, Appl

ALIGNMENTS

RESULT 1
US-09-761-288-37/c
Sequence 37, Application US/09761288
; Patent No. US200200540511
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Traupier, Raymond J
; APPLICANT: Mishra, Vishnu
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Li, Li
; TITLE OF INVENTION: No. US20020054051el Polypeptides and Nucleic Acids Encoding FILE REFERENCE: 15966-638
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/177,839
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/176,134
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/175,989
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/218,324
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/220,253
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: 60/178,191
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/178,227
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/220,590
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 37
; LENGTH: 92
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-761-288-37

Query Match Similarity 1.8%; Score 43; DB 10; Fred. No. 5.1e-11;
Best Local Similarity 100.0%; Fred. No. 5.1e-11;

RESULT 2
 Sequence 374, Application US/09764877
 Patent No. US20091714041
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 FILE REFERENCE: PCC05
 CURRENT APPLICATION NUMBER: US/09/764,877
 CURRENT FILING DATE: 2001-01-17
 PRIOR APPLICATION DATA REMOVED - refer to PALM or file wrapper
 NUMBER OF SEQ ID NOS: 4031
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 374
 LENGTH: 87
 TYPE: DNA
 ORGANISM: Homo sapiens
 S-09-764-877-3775/C

Query Match 1.88; Score 42; DB 10; Length 87;
 Best Local Similarity 100.0%; Pred. No. 1.6e-10;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 2319 TGATCCGCCACCTCGCCCTCCAAGTGGATTACAGGC 2361
 ||||||| ||||||| ||||||| ||||||| ||||||| |||||
 b 59 TGATCCGCCACCTCGCCCTCCAAGTGGATTACAGGC 17

US-09-764-877-3775/C
 Sequence 3775, Application US/09764877
 Patent No. US20091714041
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 FILE REFERENCE: PCC05
 CURRENT APPLICATION NUMBER: US/09/764,877
 CURRENT FILING DATE: 2001-01-17
 PRIOR APPLICATION DATA REMOVED - refer to PALM or file wrapper
 NUMBER OF SEQ ID NOS: 4031
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 3775
 LENGTH: 87
 TYPE: DNA
 ORGANISM: Homo sapiens
 S-09-764-877-3775/C

Query Match 1.68; Score 37; DB 10; Length 94;
 Best Local Similarity 100.0%; Pred. No. 4.2e-08;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2334 GGCTCCCAAGTGGGATTACGGCATGGCCAC 2370
 ||||||| ||||||| ||||||| ||||||| ||||||| |||||
 Db 49 GGCTCCCAAGTGGGATTACGGCATGGCCAC 85

RESULT 4
 Sequence 33, Application US/09761288
 Patent No. US20020065405A1
 GENERAL INFORMATION:
 APPLICANT: Padigaru, Muralidhara
 APPLICANT: Prayaga, Sudhirdas
 APPLICANT: Taupier, Raymond J
 APPLICANT: Mishra, Vishnu
 APPLICANT: Tchernev, Velizar
 APPLICANT: Spytek, Kimberly
 APPLICANT: Li, Li
 TITLE OF INVENTION: No. US20020065405A1el Polypeptides and Nucleic Acids Encoded by the Gene
 FILE REFERENCE: 15966-638
 CURRENT APPLICATION NUMBER: US/09/761,288
 CURRENT FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: 60/177,839
 PRIOR FILING DATE: 2000-01-25
 PRIOR APPLICATION NUMBER: 60/176,134
 PRIOR FILING DATE: 2000-01-14
 PRIOR APPLICATION NUMBER: 60/176,989
 PRIOR FILING DATE: 2000-01-13
 PRIOR APPLICATION NUMBER: 60/218,324
 PRIOR FILING DATE: 2000-07-14
 PRIOR APPLICATION NUMBER: 60/220,253
 PRIOR FILING DATE: 2000-07-24
 PRIOR APPLICATION NUMBER: 60/178,191
 PRIOR FILING DATE: 2000-01-26
 PRIOR APPLICATION NUMBER: 60/178,227
 PRIOR FILING DATE: 2000-01-26
 PRIOR APPLICATION NUMBER: 60/220,590
 PRIOR FILING DATE: 2000-07-25
 NUMBER OF SEQ ID NOS: 95
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 33
 LENGTH: 92
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-761-288-33

Query Match 1.38; Score 32; DB 10; Length 92;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2286 GTAGCCAGATGTCTGATCTCTGACCTC 2317
 ||||||| ||||||| ||||||| ||||||| ||||||| |||||
 Db 92 GTAGCCAGATGTCTGATCTCTGACCTC 61

RESULT 5
 Sequence 41, Application US/09761288
 Patent No. US20020065405A1
 GENERAL INFORMATION:
 APPLICANT: Padigaru, Muralidhara
 APPLICANT: Prayaga, Sudhirdas
 APPLICANT: Taupier, Raymond J
 APPLICANT: Mishra, Vishnu
 APPLICANT: Tchernev, Velizar
 APPLICANT: Spytek, Kimberly
 APPLICANT: Li, Li
 TITLE OF INVENTION: No. US20020065405A1el Polypeptides and Nucleic Acids Encoded by the Gene

FILE REFERENCE: 15966-638
 CURRENT APPLICATION NUMBER: US/09/761,288
 CURRENT FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: 60/177,839
 PRIOR FILING DATE: 2000-01-25
 PRIOR APPLICATION NUMBER: 60/176,134
 PRIOR FILING DATE: 2000-01-14
 PRIOR APPLICATION NUMBER: 60/175,989
 PRIOR FILING DATE: 2000-01-13
 PRIOR APPLICATION NUMBER: 60/218,324
 PRIOR FILING DATE: 2000-07-14
 PRIOR APPLICATION NUMBER: 60/220,253
 PRIOR FILING DATE: 2000-07-24
 PRIOR APPLICATION NUMBER: 60/178,191
 PRIOR FILING DATE: 2000-01-26
 PRIOR APPLICATION NUMBER: 60/178,227
 PRIOR FILING DATE: 2000-01-26
 PRIOR APPLICATION NUMBER: 60/220,590
 NUMBER OF SEQ ID NOS: 95
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 52
 LENGTH: 94
 TYPE: DNA
 ORGANISM: Homo sapiens

FILE REFERENCE: 15966-638
; CURRENT APPLICATION NUMBER: US/09/761,288
; PRIORITY FILING DATE: 2000-01-16
; PRIORITY APPLICATION NUMBER: 60/177,839
; PRIORITY FILING DATE: 2000-01-25
; PRIORITY APPLICATION NUMBER: 60/176,134
; PRIORITY FILING DATE: 2000-01-14
; PRIORITY APPLICATION NUMBER: 60/175,989
; PRIORITY FILING DATE: 2000-01-13
; PRIORITY APPLICATION NUMBER: 60/218,324
; PRIORITY FILING DATE: 2000-07-14
; PRIORITY APPLICATION NUMBER: 60/220,253
; PRIORITY FILING DATE: 2000-07-24
; PRIORITY APPLICATION NUMBER: 60/178,191
; PRIORITY FILING DATE: 2000-01-26
; PRIORITY APPLICATION NUMBER: 60/178,227
; PRIORITY FILING DATE: 2000-01-16
; PRIORITY APPLICATION NUMBER: 60/220,590
; PRIORITY FILING DATE: 2000-07-25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 41
; LENGTH: 94
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-761-288-41

Query Match 1.3%; Score 32; DB 10; Length 94;
; Best Local Similarity 100.0%; Pred. No. 1.1e-05;
; Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2286 GTAGCCAGGATGGATCTCGATCTCGACCTC 2317
Db 94 GTAGCCAGGATGGATCTCGATCTCGACCTC 63

RESULT 6
US-09-761-288-48
; Sequence 48, Application US/09761288
; Patent No. US20020065405A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Prayaga, Sudhiradas
; APPLICANT: Taupier, Raymond J
; APPLICANT: Mishra, Vishnu
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Li, Li
; TITLE OF INVENTION: No. US20020065405A1 Polypeptides and Nucleic Acids Encoding Sam
; FILE REFERENCE: 15966-638
; CURRENT APPLICATION NUMBER: US/09/761,288
; CURRENT FILING DATE: 2000-01-16
; PRIORITY APPLICATION NUMBER: 60/177,839
; PRIOR FILING DATE: 2000-01-25
; PRIORITY APPLICATION NUMBER: 60/176,134
; PRIORITY FILING DATE: 2000-01-14
; PRIORITY APPLICATION NUMBER: 60/175,989
; PRIORITY FILING DATE: 2000-01-13
; PRIORITY APPLICATION NUMBER: 60/218,324
; PRIORITY FILING DATE: 2000-07-14
; PRIORITY APPLICATION NUMBER: 60/220,253
; PRIORITY FILING DATE: 2000-07-24
; PRIORITY APPLICATION NUMBER: 60/178,191
; PRIORITY FILING DATE: 2000-01-16
; PRIORITY APPLICATION NUMBER: 60/178,227
; PRIORITY FILING DATE: 2000-01-16
; PRIORITY APPLICATION NUMBER: 60/220,590
; PRIORITY FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 47
; LENGTH: 96
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-761-288-47

Query Match 1.2%; Score 29; DB 10; Length 96;
; Best Local Similarity 100.0%; Pred. No. 0.00031;
; Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2330 CCTCGGCCTCCCAAAGTGCCTGGATTCACA 2358
Db 50 CCTCGGCCTCCCAAAGTGCCTGGATTCACA 22

RESULT 8
US-09-764-847-1866/C
; Sequence 1866, Application US/09764847
; Patent No. US200013276A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003

FILE REFERENCE: 15966-638
; CURRENT APPLICATION NUMBER: US/09/761,288
; PRIORITY FILING DATE: 2000-01-16
; PRIORITY APPLICATION NUMBER: 60/177,839
; PRIORITY FILING DATE: 2000-01-25
; PRIORITY APPLICATION NUMBER: 60/176,134
; PRIORITY FILING DATE: 2000-01-14
; PRIORITY APPLICATION NUMBER: 60/175,989
; PRIORITY FILING DATE: 2000-01-13
; PRIORITY APPLICATION NUMBER: 60/218,324
; PRIORITY FILING DATE: 2000-07-14
; PRIORITY APPLICATION NUMBER: 60/220,253
; PRIORITY FILING DATE: 2000-07-24
; PRIORITY APPLICATION NUMBER: 60/178,191
; PRIORITY FILING DATE: 2000-01-25
; PRIORITY APPLICATION NUMBER: 60/220,590
; PRIORITY FILING DATE: 2000-07-25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 48
; LENGTH: 94
; TYPE: DNA

SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1866
; LENGTH: 98
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1866

Query Match 1.2%; Score 29; DB 10; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2330 CCTGGCCTCCAAAGTGCTGGATTACA 2358
Db 29 CCTGGCCTCCAAAGTGCTGGATTACA 1

RESULT 9
US-09-764-847-1867/c
; Sequence 1867, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764.847
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION DATA REMOVED - CONSULT PALM OR FILE WRAPPER
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1867
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1867

Query Match 1.2%; Score 29; DB 10; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2330 CCTGGCCTCCAAAGTGCTGGATTACA 2358
Db 29 CCTGGCCTCCAAAGTGCTGGATTACA 1

RESULT 10
US-09-225 201 27
; Sequence 27, Application US/09225201
; Patent No. US20010007744A1
; GENERAL INFORMATION:
; APPLICANT: Chanchik, Alex
; ADDRESS: Bozicevic, Field & Francis LLP
; STREET: 200 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/859,998
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3400
; TELEFAX: 650-327-3231
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA

RESULT 11
US-09-225-201-28/c
; Sequence 28, Application US/09225201
; Patent No. US20010007744A1
; GENERAL INFORMATION:
; APPLICANT: Chanchik, Alex
; ADDRESS: Bozicevic, Field & Francis LLP
; STREET: 200 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/859,998
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3400
; TELEFAX: 650-327-3231
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA

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; FEATURE: OTHER INFORMATION: oligonucleotide primer
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-225-201-28

Query Match 1.2%; Score 28; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 40 CCTCGGCCCTCCAAAAGTGCTGGATTAC 67

RESULT 14
US-09-764-869-1719
; Sequence 1719, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/097764-869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1719
; LENGTH: 88
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-869-1719

Query Match 1.2%; Score 28; DB 10; Length 88;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2330 CCTCGGCCCTCCAAAAGTGCTGGATTAC 2357
Oy 2330 CCTCGGCCCTCCAAAAGTGCTGGATTAC 2357
Db 61 CCTCGGCCCTCCAAAAGTGCTGGATTAC 88

RESULT 15
US-09-764-860-1052/c
; Sequence 1052, Application US/09764860
; Patent No. US20020094953A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008
; CURRENT APPLICATION NUMBER: US/09764-860
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1052
; LENGTH: 84
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-860-1052

Query Match 1.1%; Score 27; DB 10; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2330 CCTCGGCCCTCCAAAAGTGCTGGATTAC 2356
Oy 2330 CCTCGGCCCTCCAAAAGTGCTGGATTAC 2356
Db 27 CCTCGGCCCTCCAAAAGTGCTGGATTAC 1

Search completed: January 11, 2003, 08:59:12
Job time : 109 secs

; FEATURE: OTHER INFORMATION: oligonucleotide primer
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-033-528-1278

Query Match 1.2%; Score 28; DB 12; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 40 CCTCGGCCCTCCAAAAGTGCTGGATTAC 2357
Qy 2330 CCTCGGCCCTCCAAAAGTGCTGGATTAC 2357

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Result No.	Query	Score	Match	Length	DB ID	Description
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c 2	gb_htc:*	41	1.7	50	9	AU104029
c 3	gb_est3:*	41	1.7	55	10	AW059824
c 4	gb_est4:*	38	1.6	53	10	AW275305
c 5	gb_est5:*	38	1.6	94	10	AW235474
c 6	gb_estfun:*	37	1.6	37	1.6	F24490
c 7	em_estba:*	8	1.6	90	17	AZ56775
c 9	em_gss_hum:*	9	1.5	54	17	BH70627
c 10	em_gss_inv:*	10	1.5	36	1.5	AZ75874
c 11	em_gss_pnt:*	11	1.5	36	1.5	AA078709
c 12	em_gss_vrt:*	12	1.5	35	1.5	AA02835
c 13	em_gss_fun:*	13	1.5	35	1.5	BE15208
c 14	em_gss_man:*	14	1.5	84	10	BE13519
c 15	em_gss_mus:*	15	1.4	96	9	AA078527
c 16	(without alignments)	16	1.3	34	1.4	AU102534
c 17	11539.710 Million cell updates/sec	17	1.3	32	1.3	NB4107
c 18		18	1.3	32	1.3	AQ92880
c 19		19	1.3	88	9	AA809831
c 20		20	1.3	50	9	R67088
c 21		21	1.3	30	1.3	F3634
c 22		22	1.3	30	1.3	T87662
c 23		23	1.3	30	1.3	BG99457
c 24		24	1.2	29	1.2	BG152006
c 25		25	1.2	29	1.2	AZ757131
c 26		26	1.2	28	1.2	AA078171
c 27		27	1.1	27	1.1	R8946
c 28		28	1.1	27	1.1	AA457759
c 29		29	1.1	27	1.1	BG527934
c 30		30	1.1	27	1.1	BG776837
c 31		31	1.1	27	1.1	BG77123
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c 33		33	1.1	27	1.1	AZ192407
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c 35		35	1.1	27	1.1	AA578401
c 36		36	1.1	26	1.1	N77004
c 37		37	1.1	26	1.1	AA807296
c 38		38	1.1	26	1.1	D20989
c 39		39	1.1	26	1.1	AA105707
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c 41		41	1.1	25	1.1	H46068
c 42		42	1.1	25	1.1	T69198
c 43		43	1.1	25	1.1	AA868654
c 44		44	1.1	25	1.1	AA912807
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c 185		185	1.1	25	1.1	RA047357
c 186		186	1.1	25	1.1	RA047357
c 18						

Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethm12.pl?t1=PM06L2=PM0-CN0155-090301-004-a12&t2=2001-03-09&t4=1>)
 Seq primer: Puc 18 forward
 High quality sequence stop: 99.

FEATURES

Location/Qualifiers	source	Matches 1..100 /organism="Homo sapiens" /db_xref="txon:3606" /clone_idb="CN015" /dev_stage="adult" /note="Organ: colon-normal; Vector: puc18; Site:1: SmaI; Site:2: SmaI; A mini-t-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent Application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions." BASE COUNT 34 a 24 c 22 g 19 t 1 others ORIGIN Query Match Score 1.8%; Best Local Similarity 100.0%; Matches 43;保守性 0; Mismatches 0; Indels 0; Gaps 0;	Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0; LOCUS AW059824 Locus LE8ell.yg DNC15 Homo sapiens cDNA, mRNA linear EST 23-AUG-2000 DEFINITION AW059824 Accession AW059824 Version AW059824.1 GI:6652146 SOURCE EST. ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 55) AUTHORS Brenner,S., Williams,S.R., Vermaess,E.H., Storck,T., Moon,K., McCollum,C., Mao,J.I., Kirchner,J.J., Elieff,S., Dubridge,R.B., Burcham,T. and Albrecht,G. TITLE In vitro cloning of complex mixtures of DNA on microbeads: Physical separation of differentially expressed cDNAs JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (4). 1665-1670 (2000) COMMENT Contact: Burcham TS LYNX Therapeutics, Inc. 25861 Industrial Blvd., Hayward, CA 94545, USA Tel: 510 670 9338 Fax: 510 670 9302 Email: timb@lynxgen.com Sequence obtained from LYNX Therapeutics Megasort technology. Collected from the down-regulated gate. High quality sequence stop: 55. Location/Qualifiers 1. .55 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_idb="DNC15" /cell_type="monocytic leukemia" /cell_line="THP-1 (TIB-102)" /note="Vector: pCR2.1; Cloning of PCR products from micro beads carrying 3' end of down-regulated cDNA. THP-1 cells non-induced (treated with DMSO only)." BASE COUNT 11 a 19 c 15 g 10 t ORIGIN Query Match Score 1.7%; Best Local Similarity 100.0%; Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0; COMMENT Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo Email: ysuzuki@ims.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,A. and Sugano S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers	source	Matches 1..50 /organism="Homo sapiens" /db_xref="txon:9606" /clone_idb="KAIRI1572" /note="Sugano Homo sapiens cDNA library" BASE COUNT 9 a 11 c 16 g 14 t ORIGIN Query Match Score 1.7%; Best Local Similarity 100.0%; Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0; LOCUS AW275505 Locus xn08f10.x1 NCL_OGAP_L15 Homo sapiens cDNA clone IMAGE:2693131_3, similar to contains Alu repetitive element, mRNA sequence. DEFINITION AW275505 Definition AW275505 Version AW275505.1 GI:6662458 SOURCE EST. ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 93) AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicbap . TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	

JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgbps@mail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution by: Greg Lennon, Ph.D.
 found through the I.M.A.G.E. Consortium/LINL at:
www-bio.lnl.gov/bbrp/image/image.html
 Seq primer: -40UP from Gibco.
 Location/Qualifiers
 1. .93
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2693131"
 /clone_id="NCI-CGAP_L15"
 /tissue_type="hepatic adenoma"
 /lab_host="DH10B"
 /note="Organ: Liver; Vector: PCMV-SPORT4; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 0.8 kb."
 19 a 23 c 23 g 28 t

FEATURES source
 BASE COUNT 19
 ORIGIN

Query Match 1.6%; Score 38; DB 10; Length 93;
 Best Local Similarity 100.0%; Pred. No. 1e-05;
 Matches 38; Conservative 0; Indels 0; Gaps 0;

DEFINITION xnl1f10.x1 NCI-CGAP_L15 Homo sapiens cDNA clone IMAGE:2693419_3,
 similar to contains Alu repetitive element; mRNA sequence.

QY 2334 GGCTTCCTCAAAGTGCGGGATTACAGGTATGAGCCACC 2371
 Db 78 GGCTTCCTCAAAGTGCGGGATTACAGGTATGAGCCACC 41

RESULT 5
 LOCUS AW235474/c
 DEFINITION xnl1f10.x1 NCI-CGAP_L15 Homo sapiens cDNA clone IMAGE:2693419_3,
 similar to contains Alu repetitive element; mRNA sequence.

ACCESSION AW235474
 VERSION EST
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE Hillier,L., Clark,N., Dubuge,T., Elliston,J., Hawkins,M., Holman,M., Hulman,M., Kucaba,T., Le,M., Lennon,G., Marras,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Wilson,A., Wohldmann,P. and Wilson,R.
 AUTHORS
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 Insert Size: 872
 High quality sequence starts: 1
 High quality sequence stop: 1
 Source: IMAGE Consortium, LINL
 This clone is available royalty-free through LINL; contact the
 IMAGE Consortium (infoimage.lnl.gov) for further information.
 Insert Length: 872
 Std Error: 0.00
 Seq primer: M13RPL
 FEATURES source
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgbps@mail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution by: Greg Lennon, Ph.D.
 found through the I.M.A.G.E. Consortium/LINL at:
www-bio.lnl.gov/bbrp/image/image.html

Possible reversed clone: polyT not found
 Seq primer: -40UP from Gibco.
 Location/Qualifiers
 1. .94
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2693419"
 /clone_id="NCI-CGAP_L15"
 /tissue_type="hepatic adenoma"
 /lab_host="DH10B"

FEATURES source
 BASE COUNT 8
 ORIGIN

/note="Organ: liver; Vector: PCMV-SPORT4; Site_1: SalI;
 Site_2: NotI; Cloned unidirectional. Primer: Oligo dT.
 Average insert size 0.8 kb."
 19 a 20 g 29 t 1 others

Query Match 1.6%; Score 38; DB 10;
 Best Local Similarity 100.0%; Pred. No. 1e-05;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DEFINITION y14dd12.r1 Soares Placenta Nb2HP Homo sapiens cDNA clone IMAGE:142295_5, similar to gbM87914 (HUMAN)N461 Human carcinoma cell-derived Alu RNA transcript, (rRNA); gd:M92424 MDM2 PROTEIN (HUMAN); mRNA sequence.

QY 2334 GGCTTCCTCAAAGTGCGGGATTACAGGTATGAGCCACC 2371
 Db 78 GGCTTCCTCAAAGTGCGGGATTACAGGTATGAGCCACC 41

RESULT 6
 LOCUS R70733
 DEFINITION y14dd12.r1 Soares Placenta Nb2HP Homo sapiens cDNA clone IMAGE:142295_5, similar to gbM87914 (HUMAN)N461 Human carcinoma cell-derived Alu RNA transcript, (rRNA); gd:M92424 MDM2 PROTEIN (HUMAN); mRNA sequence.

ACCESSION R70733
 VERSION R70733.1
 KEYWORDS EST
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE Hillier,L., Clark,N., Dubuge,T., Elliston,J., Hawkins,M., Holman,M., Hulman,M., Kucaba,T., Le,M., Lennon,G., Marras,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Wilson,A., Wohldmann,P. and Wilson,R.
 AUTHORS
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 Insert Size: 872
 High quality sequence starts: 1
 High quality sequence stop: 1
 Source: IMAGE Consortium, LINL
 This clone is available royalty-free through LINL; contact the
 IMAGE Consortium (infoimage.lnl.gov) for further information.
 Insert Length: 872
 Std Error: 0.00
 Seq primer: M13RPL
 FEATURES source
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgbps@mail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution by: Greg Lennon, Ph.D.
 found through the I.M.A.G.E. Consortium/LINL at:
www-bio.lnl.gov/bbrp/image/image.html

Possible reversed clone: polyT not found
 Seq primer: -40UP from Gibco.
 Location/Qualifiers
 1. .94
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2693419"
 /clone_id="NCI-CGAP_L15"
 /tissue_type="hepatic adenoma"
 /lab_host="DH10B"

Query Match	Score 37; DB 14; Length 37;	SOURCE	human
Best Local Similarity	100.0%	PRED.	No. 3.7e-05;
Matches 37; Conservative	0; Mismatches 0;	Indels 0;	Gaps 0;
Qy 23304 CCTCGGCCCTCCAAAGTGCCTGGATTACAGCCTGAG 2366			
Dy 1 CCTCGGCCCTCCAAAGTGCCTGGATTACAGCCTGAG 37			
RESULT 7			
LOCUS	F24490	80 bp	mRNA linear
DEFINITION	HSPD10834	HM3	Homo sapiens cDNA clone s4000013A06, mRNA sequence.
VERSION	F24490	1	GI:4810116
KEYWORDS	EST.		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Friedman,T.B.		
REFERENCE	1 (bases 1 to 80)		
AUTHORS	Lafranchi,G., Muraro,T., Caldara,F., Paccioni,B., Pallavicini,A., Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G.		
TITLE	Identification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridization		
JOURNAL	Genome Res. 6 (1), 35-42 (1996)		
MEDLINE	96276048		
COMMENT	Contact: Valeria G. CRIBI Biotechnology Centre University of Padua Via Trieste 75, 35121 Padua, Italy ABI Chromatograms and other information are available on WWW at http://grup.bio.unipd.it .		
FEATURES	Location/Qualifiers		
source	1..80		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="s4000013A06"		
	/clone_id="HM3"		
	/sex="female"		
	/tissue_type="pectoral muscle (after mastectomy)"		
	/note="Vector: pCDNAII (Invitrogen); Site 1: BstXI; Site 2: NotI; The library was constructed by G. Lafranchi. This library was not subtracted nor normalized. The first strand cDNA was primed with a biotinylated oligo dT-NotI primer (5'-biotin-AACCGGGTCGAGGCCGTTTTTTTTT-3'). The ds cDNA was sonicated and size-selected in the range 350-550 bp. The 3' specific fragments were selected by streptavidin coated magnetic beads, ligated to non-palindromic BstXI adaptors, NotI digested and directionally cloned into BstXI-NotI cut pCDNAII vector."		
BASE COUNT	18 a	21 c	19 g
ORIGIN	22 t	22 t	22 t
Query Match	Score 37; DB 14; Length 80;	LOCUS	BH770627
Best Local Similarity	100.0%	PRED.	No. 3e-05;
Matches 37; Conservative	0; Mismatches 0;	Indels 0;	Gaps 0;
Qy 23344 GGCTTCCCCAAAGTGCCTGGATTACAGCCTGAGCCAC 2370			
Dy 80 GGCTTCCCCAAAGTGCCTGGATTACAGCCTGAGCCAC 44			
RESULT 8			
LOCUS	AZ756775	90 bp	DNA linear
DEFINITION	ew01e07.x1 PAN3/FKHR CASTing Library, ew' Homo sapiens genomic clone ew01e07 random, DNA sequence.		
ACCESSION	AZ756775	1	GI:13176230
VERSION			GSS
KEYWORDS			
RESULT 9			
LOCUS	BH770627	54 bp	DNA linear
DEFINITION	LIMGtg385 MG1363 Random Sequence Tag Library Lactococcus lactis subsp.cremoris genomic, DNA sequence.		
VERSION	BH770627		
KEYWORDS			
ORGANISM	Lactococcus lactis subsp. cremoris. Lactococcus lactis subsp. cremoris. Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.		
REFERENCE	1 (bases 1 to 54)		
AUTHORS	Bolotin,A., Ehrlich,S.D. and Sorokin,A.		
JOURNAL	Studies of genomes of dairy bacteria Lactococcus lactis Sci. Aliments, (2002) In press		
COMMENT	Contact: Sorokin,A.		
	INRA INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France		
	Tel: 33 1 34 65 25 16		
	Fax: 33 1 34 65 25 21		
	Email: sorokine@jouy.inra.fr		

best homologue in strain III403 is ymbD (468)
 Class: shotgun
 High quality sequence start: 30
 High quality sequence stop: 54.

FEATURES SOURCE Location/Qualifiers

1..54 /organism="Lactococcus lactis subsp. cremoris"

/db_xref="taxon:1359"

/clone_idb="MG1363 Random Sequence Tag Library"

/note="Vector: pSKU2; Site:1: SmaI; Library of chromosomal fragments of L.lactis strain MG1363 was prepared by partial AluI digestion or by sonication."

8 a 16 c 21 g 9 t

BASE COUNT ORIGIN

Query Match Score 36; DB 17; Length 54;
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2326 CCCACCTCGGCCCTCCAAAGTGCCTGGATTACAGGC 2361

Db 18 CCCACCTCGGCCCTCCAAAGTGCCTGGATTACAGGC 53

RESULT 1.1

AA078709/c

LOCUS AA078709

DEFINITION 7TOE11 Chromosome 7 Thymus cDNA Library Homo sapiens cDNA clone

ACCESSION AA078709

VERSION AA078709.1 GI:1838204

KEYWORDS EST

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE Touchman,J.W., Bouffard,G.G., Weintraub,L.A., Idol,J.R., Wang,L., Robbins,C.M., Nussbaum,J.C., Lovett,M. and Green,E.D.

TITLE 2006 expressed-sequence tags derived from human chromosome 7-enriched cDNA libraries

JOURNAL Genome Res. 7 (3), 281-292 (1997)

COMMENT MEDLINE 9728905

CONTACT Eric D. Green

Genome Technology Branch

National Human Genome Research Institute/NIH

49 Convent Dr., MSC4431, Building 49, Room 2A08, Bethesda, MD 20892

TELEPHONE 3014024701

FAX 3014024735

EMAIL egreen@nhgri.nih.gov

PLACE 01 row: E column: 11

SEQ PRIMER -21M13 (ABI)

LOCATION/QUALIFIERS 1..74

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_idb="7TOE11"

/sex="Male"

/lab_host="DH10B"

/note="Vector: PGEM-T Easy; Human genomic DNA was partially digested with Sau3AI, ligated to ds linkers, and enriched for binding to human PAXDQ+ protein using a Whole Genome PCR-based strategy. DNA fragments containing putative PAXDQ+ binding sites were amplified by PCR and cloned into PGEM-T Easy (Promega). The ligation products were transformed into DH10B electrocompetent cells (Life Technologies)."

FEATURES SOURCE

1..61 /organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_idb="ev10d06"

/clone_idb="PAX3 CASTING Library 'ev'"

/sex="Male"

/lab_host="DH10B"

/note="Vector: PGEM-T Easy; Human genomic DNA was partially digested with Sau3AI, ligated to ds linkers, and enriched for binding to human PAXDQ+ protein using a Whole Genome PCR-based strategy. DNA fragments containing putative PAXDQ+ binding sites were amplified by PCR and cloned into PGEM-T Easy (Promega). The ligation products were transformed into DH10B electrocompetent cells (Life Technologies)."

BASE COUNT ORIGIN

11 a 22 c 16 g 12 t

FEATURES SOURCE

1..59 /organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_idb="NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548134"

BASE COUNT ORIGIN

59 bp mRNA

DEFINITION zn21g12.s1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone similar to contains Alu repetitive

Query Match Score 36; DB 17; Length 61;
 Best Local Similarity 100.0%; Pred. No. 9e-05;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2326 CCCACCTCGGCCCTCCAAAGTGCCTGGATTACAGGC 2361
 Db 18 CCCACCTCGGCCCTCCAAAGTGCCTGGATTACAGGC 53

RESULT 1.1
 AA078709/c
 LOCUS AA078709
 DEFINITION 7TOE11 Chromosome 7 Thymus cDNA Library Homo sapiens cDNA clone

ACCESSION AA078709
 VERSION AA078709.1 GI:1838204

KEYWORDS EST

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 61)

REFERENCE Barber,T.D., Barber,M.C., Tomescu,O., Barr,F.G., Ruben,S. and Friedman,T.B.

AUTHORS Barber,T.D., Barber,M.C., Tomescu,O., Barr,F.G., Ruben,S. and Friedman,T.B.

TITLE Identification of Target Genes Regulated by PAX3 and PAX3--FKHR in Embryogenesis and Alveolar Rhabdomyosarcoma

JOURNAL Genomics 79 (3), 278-284 (2002)

COMMENT CONTACT Friedman,TB

Laboratory of Molecular Genetics

National Institute on Deafness and Other Communication Disorders,
 National Institutes of Health
 5 Research Court, Room 2A-15, Rockville, MD 20850, USA

Tel: 301 496 7882

Email: friedman@lcdc.nih.gov

Plate: 10 row: d column: 06

Seq primer: -21M13 forward primer (ABI)

Class: random Plasmid subclone.

LOCATION/QUALIFIERS 1..61

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_idb="ev10d06"

/clone_idb="PAX3 CASTING Library 'ev'"

/sex="Male"

/lab_host="DH10B"

/note="Vector: PGEM-T Easy; Human genomic DNA was partially digested with Sau3AI, ligated to ds linkers, and enriched for binding to human PAXDQ+ protein using a Whole Genome PCR-based strategy. DNA fragments containing putative PAXDQ+ binding sites were amplified by PCR and cloned into PGEM-T Easy (Promega). The ligation products were transformed into DH10B electrocompetent cells (Life Technologies)."

FEATURES SOURCE

1..59 /organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_idb="NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548134"

BASE COUNT ORIGIN

11 a 22 c 16 g 12 t

FEATURES SOURCE

1..59 /organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_idb="NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548134"

BASE COUNT ORIGIN

59 bp mRNA

DEFINITION zn21g12.s1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone similar to contains Alu repetitive

element; mRNA sequence.
 ACCESSION AA082335
 VERSION 1
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE Hillier,L., Lemion,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
 Chissoe,S., Diehr,N., Dubroff,A., Favello,A., Gish,W., Hawkins
 M., Holtzman,M., Kucaba,T., Lacy,M., Le,M., Mardis,E., Moore
 B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfsing,T.,
 Scheibenbogen,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E.,
 Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Maura,M.
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)

JOURNAL 9704478
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu

This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -40N13 fwd. from Amersham.

FEATURES source
 1. 59 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="GDB:3926650"
 /db_xref="Caxon:9606"
 /clone IMAGE:54134
 /clone.lib="Stratagene neuroepithelial cells"
 /dev_stage="NTera 2/RA+MI neuroepithelial cells"
 /lab_host="SOLR (kanamycin resistant)"
 /note="Vector: PBluescript SK- Site: 1; ECORI: Site-2:
 XbaI; Cloned unidirectionally Primer: Oligo dT, NT2
 (NTera-2/c1-D1) precursor cells induced with Retinoic
 Acid for 1 week, followed by 3 weeks in mitotic inhibitors
 (Replate #2); Average insert size: 1.1 kb; Uni-ZAP XR
 Vector; ~5' adaptor sequence: 5'-GAATTCGGCACGAG 3'-,
 adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTT 3'-
 18 t

BASE COUNT 11 a 14 c 16 g 21 t
 ORIGIN

Query Match Score 1.5%; DB 9; Length 59;
 Best Local Similarity 100.0%; Pred. No. 0.00025;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
 AA078527
 LOCUS AA078527
 DEFINITION 7P05B09 Chromosome 7 Placental cDNA Library Homo sapiens CDNA CLONE
 QY 2290 GCCAGGATGGTCTCGATCTCTGCACCTCTGATCC 2324
 AA078527
 Db 59 GCCAGGATGGTCTCGATCTCTGACCTCTGATCC 25

Query Match Score 1.5%; DB 10; Length 84;
 Best Local Similarity 100.0%; Pred. No. 0.00023;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
 AA078527
 LOCUS AA078527
 DEFINITION 7P05B09 Chromosome 7 Placental mRNA Sequence
 QY 2290 GCCAGGATGGTCTCGATCTCTGCACCTCTGATCC 2324
 AA078527
 Db 59 GCCAGGATGGTCTCGATCTCTGACCTCTGATCC 25

Query Match Score 1.5%; DB 10; Length 84;
 Best Local Similarity 100.0%; Pred. No. 0.00023;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
 AA078527
 LOCUS AA078527
 DEFINITION 7P05B09 Chromosome 7 Placental mRNA Sequence
 QY 2290 GCCAGGATGGTCTCGATCTCTGCACCTCTGATCC 2324
 AA078527
 Db 59 GCCAGGATGGTCTCGATCTCTGACCTCTGATCC 25

Query Match Score 1.5%; DB 9; Length 59;
 Best Local Similarity 100.0%; Pred. No. 0.00025;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
 BE515208
 LOCUS BE515208
 DEFINITION 601235939F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608045 5',
 mRNA sequence.

ACCESSION BE515208
 VERSION 1
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 84)
 NIH-MGC http://mcg.ncbi.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov

/note="Organ: placenta; Vector: pAMP10; cDNA was generated from cytoplasmic RNA using a mixture of random DNA hexamers and oligo(dT). From this pool of cDNA, human chromosome 7-enriched cDNA was isolated by direct cDNA selection using chromosome 7 genomic DNA (cosmids). The resulting direct-selected cDNA was cloned into plasmid vector using a non-directional uracil DNA glycosylase (UDG)-mediated cloning strategy."

BASE COUNT 25 a 29 C 20 G 22 t
ORIGIN

Query Match 1.5%; Score 35; DB 9; Length 96;
Best Local Similarity 100.0%; Pred. No. 0.00022;
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Qy 2337 CTCCCCAAAGTGCTGGATACAGGCATGCCACC 2371
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RESULT 15

AU102534 AU102534 50 bp mRNA linear EST 30-AUG-2001
DEFINITION AU102534 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ADSH00605, mRNA sequence.

ACCESSION AU102534

VERSION AU102534.1 GI:13552055

KEYWORDS EST.

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Sugano,A. and Sugano,S.

TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072

COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
Email: y Suzuki@ims.u-tokyo.ac.jp

Suzuki,Y., Yoshitono-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES Location/Qualifiers
source
1..50

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ADSH00605"

/clone_id="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and dimethylfumarate treated U937 cells"

BASE COUNT 10 a 18 c 13 g 9 t
ORIGIN

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Db 10 CCTCGGGCCTCCCAAAGTGCTGGATTACAGGCAT 43

Search completed: January 11, 2003, 07:04:15
Job time : 3334 secs

